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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,003

DATE: 07/30/2001

TIME: 12:09:42

Input Set : N:\Cr3\RULE60\09758003.txt

Output Set: N:\CRF3\07302001\I758003.raw

## SEQUENCE LISTING

ENTERED

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: BACHWAL, VINAY K

4 HUANG, JIANNING

5 HUI, HAILING

6 GEDDOEL, DAVID V

7 (ii) TITLE OF INVENTION: RFP: NOVEL HUMAN PROTEIN INVOLVED IN

8 TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING

9 ASSAYS

10 (iii) NUMBER OF SEQUENCES: 1

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP

13 (B) CLIENT: US DENISE DEIVE

14 (C) CITY: HILLSBOROUGH

15 (D) STATE: CALIFORNIA

16 (E) COUNTRY: USA

17 (F) ZIP: 94010

18 (v) COMPUTER READABLE FORM:

19 (A) MEDIUM TYPE: Floppy disk

20 (B) COMPUTER: IBM PC compatible

21 (C) OPERATING SYSTEM: PC-DOS,MS-DOS

22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

23 (vi) CURRENT APPLICATION DATA:

C--> 24 (A) APPLICATION NUMBER: US/09/758,003

C--> 25 (B) FILING DATE: 09-Jan-2001

26 (C) CLASSIFICATION:

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: 09/132,113

29 (B) FILING DATE:

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: OSMAN, RICHARD A.

32 (B) REGISTRATION NUMBER: 36,627

33 (C) REFERENCE/DOCKET NUMBER: T95-006-1

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: (650) 343-4341

36 (B) TELEFAX: (650) 343-4342

37 (2) INFORMATION FOR SEQ ID NO: 1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 2016 base pairs

40 (B) TYPE: nucleic acid

41 (C) STRANDEDNESS: double

42 (D) TOPOLOGY: linear

43 (ii) MOLECULE TYPE: cDNA

44 (ix) FEATURE:

45 (A) NAME/KEY: CDS

46 (B) LOCATION: 1...1015

47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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52	ATG	CAA	CCA	GAT	ATG	TTC	TTG	AAT	GTC	ATT	AAG	ATG	AAA	TCC	AAT	GAC	48
53	Met	Gln	Pro	Asp	Met	Ser	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ser	Asp	
54	1			5					10					15			
55	TTC	CTG	GAG	AGT	ACA	GAA	CTG	GAC	AGC	GGA	GGC	TTT	GGG	AAG	GTG	TCT	96
56	Phe	Leu	Gln	Ser	Ala	Glu	Leu	Asp	Ser	Gly	Gly	Phe	Gly	Lys	Val	Ser	
57				20					25					30			
58	CTG	TGT	TTC	CAC	AGA	AAC	GAG	GGA	CTC	ATG	ATC	ATG	AAA	ACA	GTG	TAC	144
59	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr	
60			35					40					45				
61	AAG	GGG	CCC	AAT	TGC	ATT	GAG	CAC	AAT	GAG	GGT	CTC	TTG	ACG	GAG	GGG	192
62	Lys	Gly	Pro	Asn	Lys	Ile	Gln	His	Asn	Gln	Ala	Leu	Leu	Ile	Gln	Ala	
63		50				55					60						
64	AAG	ATG	ATG	AAC	AGA	CTG	AGA	CAC	AGC	GGG	GTG	GTG	AAG	CTC	CTG	GGC	240
65	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Leu	Gly	
66		65			70				75				80				
67	GTC	ATC	ATA	GAG	GAA	GGG	AAG	TAC	TCC	CTG	GTG	ATG	GAG	TAC	ATG	GAG	288
68	Val	Ile	Ile	Gln	Gln	Gly	Lys	Tyr	Ser	Leu	Val	Met	Gln	Tyr	Met	Gln	
69				85					90				95				
70	AAG	GGC	AAC	CTG	ATG	CAC	GTG	CTG	AAA	GCC	GAG	ATG	AGT	ACT	CCG	CTT	336
71	Lys	Gly	Asn	Leu	Met	His	Val	Leu	Lys	Ala	Gln	Met	Ser	Thr	Pro	Leu	
72			100						105				110				
73	TCT	GTA	AAA	GGA	AGG	ATA	ATT	TTG	GAA	ATC	ATT	GAA	GGA	ATG	TGC	TAC	384
74	Ser	Val	Lys	Gly	Arg	Ile	Ile	Leu	Gln	Ile	Ile	Gln	Gly	Met	Cys	Tyr	
75			115					120					125				
76	TTA	CAT	GGA	AAA	GGC	GTG	ATA	CAC	AAG	GAC	CTG	AAG	CCT	GAA	AAT	ATC	432
77	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Asp	Leu	Lys	Pro	Gln	Asn	Ile	
78		130				135					140						
79	CTT	GTT	GAT	AAT	GAC	TTC	CAC	ATT	AAG	ATC	GCA	GAC	CTC	GGC	CTT	GCC	480
80	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
81	145				150				155				160				
82	TCC	TTT	AAG	ATG	TGG	AGC	AAA	CTG	AAT	AAT	GAA	GAG	CAC	AAT	GAG	CTG	528
83	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Gln	Gln	His	Asn	Gln	Leu	
84			165						170				175				
85	AGG	GAA	GTG	GAC	GGC	ACC	GCT	AAG	AAG	AAT	GGC	GGC	ACC	CTC	TAC	TAC	576
86	Arg	Glu	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr	
87			180					185					190				
88	ATG	GCG	CCC	GAG	CAC	CTG	AAT	GAC	GTC	AAC	GCA	AAG	CCC	ACA	GAG	ATG	624
89	Met	Ala	Pro	Gln	His	Leu	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Gln	Lys	
90		195					200					205					
91	TGG	GAT	GTG	TAC	AGC	TTT	GCT	GTA	GTA	CTC	TGG	GCG	ATA	TTT	GCA	AAT	672
92	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Val	Leu	Trp	Ala	Ile	Phe	Ala	Asn	
93		210				215					220						
94	AAG	GAG	CCA	TAT	GAA	AAT	GCT	ATC	TGT	GAG	CAG	TAG	TTG	AIA	ATG	TGC	720
95	Lys	Gln	Pro	Tyr	Gln	Asn	Ala	Ile	Cys	Gln	Gln	Gln	Leu	Ile	Met	Cys	
96		225				230				235			240				
97	ATA	AAA	TCT	GGG	AAG	AGG	CCA	GAT	GTG	GAT	GAC	ATC	ACT	GAG	TAC	TGC	768
98	Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Gln	Tyr	Cys	
99			245						250				255				
100	CCA	AGA	GAA	ATT	ATC	AGT	CTC	ATG	AAG	CTC	TGC	TGG	GAA	GGG	AAT	CCG	816

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```

101 Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
102          260          265          270
103 GAA GCT CGG CTG ATA TTT GCT GGT ATT GAA GAA AAA TTT AGG CCT TTT      364
104 Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
105          275          280          285
106 TAT TTA AGT CAA TTA GAA GAA AGT GTA GAA GAG GAG CTG AAG AGT TTA      412
107 Tyr Leu Ser Glu Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Ser
108          290          295          300
109 AAG AAA GAG TAT TCA AAC GAA AAT GCA GTT CTG AAG ACA ATT CAG TTT      460
110 Lys Lys Glu Tyr Ser Asn Ala Asn Ala Val Val Lys Arg Met Glu Ser
111          305          310          315
112 CTT CAA GTT GAT TGT GTG GCA GTA CCT TCA AGC CCG TCA AAT TCA GTC      1008
113 Leu Glu Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
114          320          325          330
115 ACA GAA CAG CTT GGT TCA CTG CAC AGT TCC CAG GGA GTT AGG ATG GGT      1056
116 Thr Glu Glu Pro Gly Ser Leu His Ser Ser Glu Gly Leu Gly Met Gly
117          340          345          350
118 CCT GTG GAG GAG TCC TGG TTT GGT CCT TCC CTG GAG CAC TCA CAA GAA      1104
119 Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Glu Glu
120          355          360          365
121 GAG AAT GAG CCG AGC CTG CAG AGT AAA CTC CAA GAG GAA GCG AAC TAC      1152
122 Glu Asn Glu Pro Ser Leu Glu Ser Lys Leu Glu Asp Glu Ala Asn Tyr
123          370          375          380
124 CAT CTT TAT GGC AGC CGC ATG GAC AGG CAG AGC AAA CAG CAG CCC AGA      1200
125 His Leu Tyr Gly Ser Arg Met Asp Arg Glu Thr Lys Glu Glu Pro Arg
126          385          390          395
127 CAG AAT GTG GCT TAC AAC AGA GAG CAG GAA AGG AGA CCG AGG GTC TCC      1248
128 Glu Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
129          400          405          410
130 CAT GAC CCT TTT GCA CAG CAA AGA CCT TAC GAG AAT TTT CAG AAT ACA      1296
131 His Asp Pro Phe Ala Glu Glu Arg Pro Tyr Glu Asn Phe Glu Asn Thr
132          420          425          430
133 GAG GGA AAA GGC ACT GTT TAT TCC AGT GCA GCG AGT CAT GGT AAT GCA      1344
134 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
135          435          440          445
136 GTG CAC CAG CCG TCA GGG CTC ACC AGC CAA GCT CAA GTA CTG TAT CAG      1392
137 Val His Glu Pro Ser Gly Leu Thr Ser Glu Pro Glu Val Leu Tyr Glu
138          450          455          460
139 AAC AAT GGA TTA TAT AGC TCA CAT GGC TTT GGA ACA AGA CCA CTG GAT      1440
140 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
141          465          470          475
142 CCA GGA ACA GCA GGT CCC AGA GTT TGG TAC AGG CCA ATT CCA AGT CAT      1488
143 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
144          480          485          490
145 ATG CCT AGT CTG CAT AAT ATC CCA GTG CCT GAG ACC AAC TAT CTA GGA      1536
146 Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly
147          495          500          505
148 AAT ACA CCG ACC ATG CCA TTC AGC TCC TTC CCA CCA ACA GAT GAA TCT      1584
149 Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser

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```

150          515          520          525
151 ATA AAA TAT ACC ATA TAC AAT AGT AAT GAC ATT CAG ATT GGA GCG TAC      1632
152 Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Thr
153          530          535          540
154 AAT TAT ATG GAG ATT GGT GGG ACG AST TTA TCA CTA CTA GAT AGC ACA      1680
155 Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr
156 545          550          555          560
157 AAT AAT AAC TTC AAA GAA GAG CCA GGT GGT AAG TAC GAA GGT ATC TTT      1728
158 Asn Thr Asn Phe Lys Gln Gln Pro Ala Ala Lys Tyr Gln Ala Ile Phe
159          565          570          575
160 GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA      1776
161 Asp Asn Thr Thr Ser Leu Phe Asp Lys His Leu Asp Pro Ile Arg Glu
162          580          585          590
163 AAT CTG GGA AAG TAC TGG AAA AAC TGT GGT GGT AAA CTG GGC TTC ACA      1824
164 Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr
165          595          600          605
166 CAG CTT CAG ATT GAT GAA ATT GAT GAT GAT TAT GAG CGA GAT GGA CTG      1872
167 Gln Ser Gln Ile Asp Gln Ile Asp His Asp Tyr Gln Arg Asp Gly Leu
168          610          615          620
169 AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC      1920
170 Lys Gln Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Gln Gly
171 6.5          630          635          640
172 ATA AAG GGA GCG ACG CTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT      1968
173 Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys
174          645          650          655
175 TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC      2013
176 Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn
177          660          665          670
178 TAA      2016
180 (2) INFORMATION FOR SEQ ID NO: 2:
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 671 amino acids
183 (B) TYPE: amino acid
184 (C) TOPOLOGY: linear
185 (ii) MOLECULE TYPE: protein
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
187 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp
188 1 10 15
189 Phe Leu Gln Ser Ala Gln Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
190 20 25 30
191 Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr
192 35 40 45
193 Lys Gly Pro Asn Cys Ile Gln His Asn Glu Ala Leu Leu Glu Glu Ala
194 50 55 60
195 Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
196 65 70 75 80
197 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
198 85 90 95
199 Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu

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```

200          100          105          110
201 Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Gln Gly Met Cys Thr
202          115          120          125
203 Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Gln Asn Ile
204          130          135          140
205 Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala
206 145          150          155          160
207 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
208          165          170          175
209 Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
210          180          185          190
211 Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
212          195          200          205
213 Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
214          210          215          220
215 Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
216 225          230          235          240
217 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Gln Tyr Cys
218          245          250          255
219 Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
220          260          265          270
221 Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
222          275          280          285
223 Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
224          290          295          300
225 Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
226 305          310          315          320
227 Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
228          325          330          335
229 Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
230          340          345          350
231 Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu
232          355          360          365
233 Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
234          370          375          380
235 His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
236 385          390          395          400
237 Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
238          405          410          415
239 His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
240          420          425          430
241 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
242          435          440          445
243 Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
244          450          455          460
245 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
246 465          470          475          480
247 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
248          485          490          495

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/758,003

DATE: 07/30/2001

TIME: 10:09:43

Input Set : N:\Crf3\RULE60\09758003.txt

Output Set: N:\CRF3\07302001\I758003.raw

L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]